Network Project Proposal
CptS 591 Spring 2019

Matthew Mietchen
Hitesh Bahar

Project Description:

Healthcare delivery in most industrialized nations endure a common challenge toward antimicrobial resistant pathogens causing complications with patient recovery and costly healthcare resources. An antimicrobial resistant pathogen such as MRSA or methicillin resistant staphylococcus aureus, is one such pathogen that continues to complicate treatment, extend hospital stay, and in some cases, cause fatalities.

MRSA infections are known to move throughout hospitals and other healthcare facilities through contact with colonized and contaminated individuals. Healthcare workers are thought to be a main contamination component simply due to their exposure in the healthcare setting. Contamination of a healthcare worker may lead to the colonization, or pathogen harboring without causing infection, of patients. Once a patient is colonized, several factors including compromised immune systems or invasive procedures may lead to an infection.

Currently, there are several treatment options for MRSA, however, hospital epidemiology continues to study the question of how to reduce the spread of the pathogen and ultimately the rate of colonization and infection. One current method to study the transmission if such pathogens is to develop mathematical models to explore different interventions or simply try to understand how the pathogens moves throughout a population over time. Performing real-time studies such as patient cohorts and case-control studies within a hospital setting can be very costly and difficult to implement. Models are one method to possibly give insight and test hypotheses.

One very important question in hospital infection control has been focused around the idea of infected or colonized patients being transferred not only throughout a hospital but also between hospitals. These hospital transfers pose important questions to be further understood in order to begin to propose interventions or policy changes to attempt to reduce MRSA infections.

Healthcare for many patients is an elaborate connection of multiple facilities during the treatment of many patients. Acute-care hospitals, long-term care facilities, emergency departments, and therapy centers may be a part of a patient's care network. Therefore, a network of healthcare facilities could potentially be contributing to an overall prevalence of a pathogen such as MRSA. If patients who are colonized or infected are then transferred to a different hospital, how does this affect the overall colonization rates of the hospital? This question will be explored by constructing a meta-population network model of healthcare facilities involving the spread and colonization of MRSA.

A metapopulation model is comprised of a network of sub-populations that have a high degree of interaction within the sub-population and a low degree of interaction between those population, but an interaction nonetheless. In the proposed model, a network of hospitals or healthcare facilities will be constructed to each have their own epidemic model within the hospital only connected by the transfer of patients between hospitals. The main question here being, does an outbreak of MRSA within a hospital affect the overall prevalence of MRSA in other facilities or the network in general. Various types of networks will be attempted to be studied and compared as well as the structure of those networks, however, the epidemic models for each hospital will remain equal with the assumption that MRSA will spread the same within any given location or space in the healthcare system.

Methods:

Two different network classes will be generated to compare epidemic acquisitions. A Erdos-Renyi random graph and Barabasi preferential graph will give insight to dynamics of real-world hospital networks. The random graph allows inference to be made from several different types of hospital structures, however, the Barabasi graph very well may represent an actual hospital transfer network as one main acute care facility will be transferring patients out to many facilities throughout the community.

Hospitals will be represented as nodes in the network and each hospital will have an epidemic model embedded or associated with that hospital. However, for this project, we will assume that the spread of MRSA and all parameters will be the same and therefore will implement the same epidemic model for each subpopulation or node. Our main interest will be to observe the behavior of the network and how MRSA may move throughout the entire network. Previous hospital models have been studied and several parameters will be implemented into the model. Some network parameters will be implemented. For example, there will be a probability associated with a patient transfer, however, the subtraction of a patient from hospital A will result in an addition of a patient in hospital B.

For the project, we will use the EpiModel package in R for initial model creation and simulations. We may attempt to build the entire network of models in Python in order to simulate the epidemics across the network using Kamiak job submissions but this will be dependant upon the level of simulations determined to be required for the model results. If sufficient results are generated within EpiModel without expensive computation costs, this project may be accomplished in the R package only.

Data:

No data will need to be collected as the results will be simulated from the network model. Pathogen [MRSA] acquisitions will be counted for each node over the duration of one year and simulated across many years in order to cover the possibilities of the network space.

Background:

In today's world, transmission of disease often takes place with the help of carrier, mostly by human to human via contacts. This can be studied with the help of epidemiology. In the metapopulation network, different physical locations are taken into consideration as nodes and edges represents humans relocating from one location to another, such as a patient transfer between hospitals. A common example of this could be considered as Ebola [1], MRSA [2]. There are many methods to form metapopulation colonization, like using the Lagrangian approach, which uses parameter p_i for any given time i, where p determines the spread of pathogens in metapopulation. Also there are other methods, like shortest path tree which uses average transmission pathways between the populations. Other models like calculating the distance and using the Monte Carlo method in the Maximum Likelihood, for creating simulations and observing the flow of pathogens/disease in the metapopulations via human contacts or humans itself. Epidemic models such as the SIS/SIR models have been used for all the above methods discussed.

Plan:

Week 1

Review the various model components and statistical packages. Begin model selection and determine meeting times for project work and collaboration.

Week 2

Build and implement the subpopulation model.

Week 3

Code the subpopulation model into a larger network to begin work on network model simulations. Perform data analysis on subpopulation model simulations.

Week 4

Finish all simulations and data analysis. Complete project and begin project presentation. Present project in class on assigned date. Begin writing the final report.

Week 5

Finish writing final report for submission.

References:

[1] Anzo-Hernández, A., et al. “The Risk Matrix of Vector-Borne Diseases in Metapopulation Networks and Its Relation with Local and Global R0.” Communications in Nonlinear Science and Numerical Simulation, vol. 68, 2019, pp. 1–14., doi:10.1016/j.cnsns.2018.06.006.

[2] Goldstein, Neal D., et al. “A Network Model of Hand Hygiene: How Good Is Good Enough to Stop the Spread of MRSA?” Infection Control & Hospital Epidemiology, vol. 38, no. 08, 2017, pp. 945–952., doi:10.1017/ice.2017.116.

[3] Lee, Bruce Y., et al. “Modeling the Spread of Methicillin-Resistant Staphylococcus Aureus (MRSA) Outbreaks throughout the Hospitals in Orange County, California.” Infection Control & Hospital Epidemiology, vol. 32, no. 06, 2011, pp. 562–572., doi:10.1086/660014.

[4] Wang, Jian-Bo, et al. “Identifying Spatial Invasion of Pandemics on Metapopulation Networks Via Anatomizing Arrival History.” IEEE Transactions on Cybernetics, vol. 46, no. 12, 2016, pp. 2782–2795., doi:10.1109/tcyb.2015.2489702.